AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1-48 (Canceled).

49. (currently amended) A method performed in a computer of producing a genome specific stoichiometric matrix of a microbe, comprising:

obtaining a plurality of DNA sequences in ~~of~~ a genome, wherein said plurality comprises a number of DNA sequences in a genome sufficient to produce an *in silico* representation of a microbe;

determining open reading frames of genes in said plurality of DNA sequences~~microbe~~; assigning a function to proteins encoded by said open reading frames by determining the homology of said open reading frames to gene sequences encoding proteins of known function;

determining which of said open reading frames correspond to metabolic genes by determining if the assigned function of said proteins is involved in cellular metabolism;

determining substrates, products and stoichiometry for each of said metabolic genes; and

producing a genome specific stoichiometric matrix of said microbe from said substrates, products and stoichiometry.

50. (previously presented) The method of Claim 49, wherein said microbe is *Escherichia coli.*

51. (previously presented) The method of Claim 49, wherein said genes involved in cellular metabolism comprise genes involved in central metabolism, amino acid metabolism, nucleotide metabolism, fatty acid metabolism, lipid metabolism, vitamin and cofactor biosynthesis, energy and redox generation or carbohydrate assimilation.

52. (previously presented) The method of Claim 49, wherein assigning a function comprises performing a homology search using the Basic Local Alignment Search Tool (BLAST).

53. (previously presented) A method of producing an *in silico* representation of a microbe in a computer, comprising:

producing a genome specific stoichiometric matrix of said microbe by the method of Claim 49;

determining a metabolic demand corresponding to a biomass composition of said microbe;

calculating uptake rates of metabolites of said microbe; and

combining said metabolic demands and said uptake rates with said stoichiometric matrix to produce an *in silco* representation of said microbe.

54. (currently amended) A method of simulating a metabolic capability of an *in silico* representation of a microbe, comprising~~The method of Claim 53, further comprising performing a flux balance analysis on said *in silico* representation.~~:

producing a genome specific stoichiometric matrix of said microbe by the method of claim 49;

determining a metabolic demand corresponding to a biomass composition of said microbe;

calculating uptake rates of metabolites of said microbe;

combining said metabolic demands and said uptake rates with said stoichiometric matrix to produce an *in silco* representation of said microbe, and

performing a flux balance analysis on said *in silico* representation.

Claim 55 (cancelled).

56. (previously presented) The method of Claim 53, wherein said uptake rates are calculated by measuring the depletion of substrate from growth media of said microbe.

57. (currently amended) A method performed in a computer for producing a genome specific stoichiometric matrix of a microbe, comprising:

a) providing a ~~the~~ nucleotide sequence of a metabolic gene in the microbe;

~~b) identifying the open reading frame of the metabolic gene to determine the corresponding gene product~~;

~~c) assigning a function to the metabolic gene product based on its nucleotide or amino acid homology to other, known metabolic gene products~~;

b~~d~~) determining ~~the~~ substrates, products and stoichiometry for said metabolic gene product based on its assigned function;

c~~e~~) repeating steps a) and b) ~~to d)~~ for a plurality of metabolic genes of said microbe sufficient to produce an *in silico* representation~~until the substrates, products and stoichiometry of the metabolic genes in said microbe are known~~; and

d~~f~~) producing a genome specific stoichiometric matrix from said substrates, products and stoichiometry of the metabolic genes product in said microbe.

58. (previously presented) The method of Claim 57, wherein the microbe is *Escherichia coli.*

59. (previously presented) The method of Claim 57, wherein said metabolic gene is selected from the group consisting of: genes involved in central metabolism, amino acid metabolism, nucleotide metabolism, fatty acid metabolism, lipid metabolism, vitamin and cofactor biosynthesis, energy and redox generation and carbohydrate assimilation.

60. (previously presented) The method of Claim 57, wherein assigning a function comprises performing a homology search using the Basic Local Alignment Search Tool (BLAST).

61. (previously presented) A method performed in a computer of producing an *in silico* representation of a microbe, comprising:

producing a genome specific stoichiometric matrix of said microbe by the method of Claim 57;

determining a metabolic demand corresponding to a biomass composition of said microbe;

calculating uptake rates of metabolites of said microbe; and

combining said metabolic demands and said uptake rates with said

stoichiometric matrix to produce an *in silico* representation of said microbe.

62. (previously presented) The method of Claim 61, wherein said microbe is *Escherichia coli.*

63. (cancelled)

64. (previously presented) The method of Claim 61, wherein said uptake rates are calculated by measuring the depletion of substrate from growth media of said microbe.

65. (currently amended) A method of simulating a metabolic capability of an *in silico* representation of a microbe, comprising~~The method of Claim 61, further comprising performing a flux balance analysis on said *in silico* representation of said microbe.~~

producing a genome specific stoichiometric matrix of said microbe by the method of claim 61;

determining a metabolic demand corresponding to a biomass composition of said microbe;

calculating uptake rates of metabolites of said microbe, and

combining said metabolic demands and said uptake rates with said stoichiometric matrix to produce an *in silico* representation of said microbe.